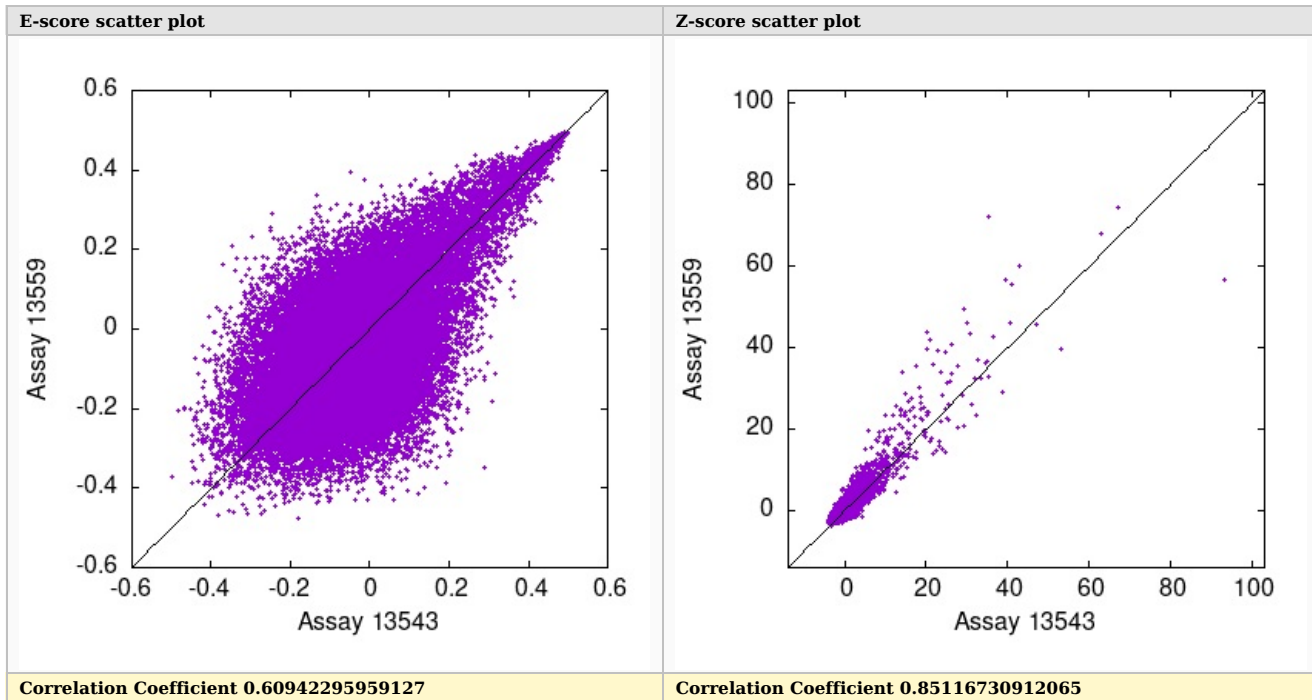


QC report



Top scoring motifs for Assay 13543

Protein ID: pTH14290.1 Gene: CGGBP1.FL Domain: Unknown Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CGGCGGCA	0.49916	TGCCGCCG--	CGGCGGCA	93.36270	TGCCGCCG--
GCCGCCGA	0.49833	-GCCGCCGA-	CGCCGCCG	67.19254	CGCCGCCG--
CGCCGCCG	0.49770	CGCCGCCG--	GCCGCCGA	62.90803	-GCCGCCGA-
GCCGCCGC	0.49630	-GCCGCCGC-	GCCGCCGC	53.13536	-GCCGCCGC-
CGGCCGAA	0.49504	--CCGCCGAA	CCGCCGAA	47.25810	--CCGCCGAA
ACGGCGGC	0.49318	-GCCGCCGT-	GCCGCCGC	43.04293	-GCCGCCGC-
CGGCCGGC	0.49303	-GCCGCCGG-	ACGCCCGA	41.02491	-ACGCCCGA-
ACGCCCGA	0.49302	-ACGCCCGA-	CGCCGCCG	40.47387	CGCCGCCG--
CGCGGGCG	0.49246	CGCCGCCG--	CGCCGCAG	39.52276	CGCCGCCG--
CGCCGCAG	0.49240	CGCCGCAG--	CGCCGCCG	38.59859	--CCGCCGCCG

Top scoring motifs for Assay 13559

Protein ID: pTH14290.2 Gene: CGGBP1.FL Domain: Unknown Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CGCCGCCG	0.49670	CGCCGCCG--	CGCCGCCG	74.59760	CGCCGCCG--
GCCGCCGA	0.49533	-GCCGCCGA-	ACGGCGGC	72.24044	-GCCGCCGT-
CGCCGCAG	0.49479	CGCCGCAG--	CGCCGCCA	68.19641	-GCCGCCGA-
ACGGCGGC	0.49466	-GCCGCCGT-	GCCGCCGC	60.08075	-GCCGCCGC-
ACGCCCGA	0.49418	-ACGCCCGA-	CGCCGCAG	56.86047	CGCCGCAG--
CGGCCGCA	0.49334	TGCCGCCG--	CGCCGCCA	56.56005	TGCCGCCG--
CCGCCGAA	0.49265	--CCGCCGAA	ACGCCCGA	55.68139	-ACGCCCGA-
GCCGCCGC	0.49139	-GCCGCCGC-	GCCGCCGA	49.64600	-GCCGCCGA-
CACCGCCG	0.49131	CACCGCCG--	CGCCGCCG	46.06611	CGCCGCCG--
GCCGCAGA	0.49074	-GCCGCAGA-	CTGCCGCA	46.00378	TGCCGCAG-